PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/09/393,023A*

DATE: 12/24/1999
TIME: 04:44:53

INPUT SET: S34300.raw

> **This Raw Listing contains the General Information Section and up to the first 5 pages.**

```
1                                        SEQUENCE LISTING        ENTERED
2
3    (1)     General Information:
4
5        (i) APPLICANT: Meissner, Paul S.
6                       Coleman, Timothy A.
7
8       (ii) TITLE OF INVENTION: Human Criptin Growth Factor
9
10     (iii) NUMBER OF SEQUENCES: 7
11
12      (iv) CORRESPONDENCE ADDRESS:
13             (A) ADDRESSEE: Human Genome Sciences, Inc.
14             (B) STREET: 9410 Key West Avenue
15             (C) CITY: Rockville
16             (D) STATE: MD
17             (E) COUNTRY: USA
18             (F) ZIP: 20850
19
20       (v) COMPUTER READABLE FORM:
21             (A) MEDIUM TYPE: Floppy disk
22             (B) COMPUTER: IBM PC compatible
23             (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24             (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25
26      (vi) CURRENT APPLICATION DATA:
27             (A) APPLICATION NUMBER: US 09/393,023
28             (B) FILING DATE: 09-SEP-1999
29             (C) CLASSIFICATION:
30
31     (vii) PRIOR APPLICATION DATA:
32             (A) APPLICATION NUMBER: US 08/471,371
33             (B) FILING DATE: 06-JUN-1995
34
35    (viii) ATTORNEY/AGENT INFORMATION:
36             (A) NAME: Marks, Michelle S.
37             (B) REGISTRATION NUMBER: 41,971
38             (C) REFERENCE/DOCKET NUMBER: PF200D1
39
40      (ix) TELECOMMUNICATION INFORMATION:
41             (A) TELEPHONE: 301-309-8504
42             (B) TELEFAX: 301-309-8439
43
44
45    (2) INFORMATION FOR SEQ ID NO:1:
46
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INPUT SET: S34300.raw

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47        (i)  SEQUENCE CHARACTERISTICS:
48             (A)  LENGTH: 672 base pairs
49             (B)  TYPE: nucleic acid
50             (C)  STRANDEDNESS: single
51             (D)  TOPOLOGY: linear
52
53        (ii) MOLECULE TYPE: DNA (genomic)
54
55
56        (ix) FEATURE:
57             (A)  NAME/KEY: CDS
58             (B)  LOCATION: 1..672
59
60
61        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
62
63   ATG ACC TGG AGG CAC CAT GTC AGG CTT CTG TTT ACG GTC AGT TTG GCA      48
64   Met Thr Trp Arg His His Val Arg Leu Leu Phe Thr Val Ser Leu Ala
65    1               5                   10                  15
66
67   TTA CAG ATC ATC AAT TTG GGA AAC AGC TAT CAA AGA GAG AAA CAT AAC      96
68   Leu Gln Ile Ile Asn Leu Gly Asn Ser Tyr Gln Arg Glu Lys His Asn
69                20                  25                  30
70
71   GGC GGT AGA GGG GAA GTC ACC AAG GTT GCC ACT CAG AAG CAC CGA CAG     144
72   Gly Gly Arg Gly Glu Val Thr Lys Val Ala Thr Gln Lys His Arg Gln
73            35                  40                  45
74
75   TCA CCG CTT AAC TGG ACC TCC AGT CAT TTC GGA GAG GTG ACT GGG AGC     192
76   Ser Pro Leu Asn Trp Thr Ser Ser His Phe Gly Glu Val Thr Gly Ser
77        50                  55                  60
78
79   GCC GAG GGC TGG GGG CCG GAG GAG CCG CTC CCC TAC TCC CGG GCT TTC     240
80   Ala Glu Gly Trp Gly Pro Glu Glu Pro Leu Pro Tyr Ser Arg Ala Phe
81    65                  70                  75                  80
82
83   GGA GAG GGT GCG TCC GCG CGG CCG CGC TGC TGC AGG AAC GGC GGT ACC     288
84   Gly Glu Gly Ala Ser Ala Arg Pro Arg Cys Cys Arg Asn Gly Gly Thr
85                85                  90                  95
86
87   TGC GTG CTG GGC AGC TTC TGC GTG TGC CCG GCC CAC TTC ACC GGC CGC     336
88   Cys Val Leu Gly Ser Phe Cys Val Cys Pro Ala His Phe Thr Gly Arg
89                100                 105                 110
90
91   TAC TGC GAG CAT GAC CAG AGG CGC AGT GAA TGC GGC GCC CTG GAG CAC     384
92   Tyr Cys Glu His Asp Gln Arg Arg Ser Glu Cys Gly Ala Leu Glu His
93            115                 120                 125
94
95   GGA GCC TGG ACC CTC CGC GCC TGC CAC CTC TGC AGG TGC ATC TTC GGG     432
96   Gly Ala Trp Thr Leu Arg Ala Cys His Leu Cys Arg Cys Ile Phe Gly
97        130                 135                 140
98
99   GCC CTG CAC TGC CTC CCC CTC CAG ACG CCT GAC CGC TGT GAC CCG AAA     480
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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/393,023A

INPUT SET: S34300.raw

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100   Ala Leu His Cys Leu Pro Leu Gln Thr Pro Asp Arg Cys Asp Pro Lys
101   145             150             155             160
102
103   GAC TTC CTG GCC TCC CAC GCT CAC GGG CCG AGC GCC GGG GGC GCG CCC      528
104   Asp Phe Leu Ala Ser His Ala His Gly Pro Ser Ala Gly Gly Ala Pro
105               165             170             175
106
107   AGC CTG CTA CTC TTG CTG CCC TGC GCA CTC CTG CAC CGC CTC CTG CGC      576
108   Ser Leu Leu Leu Leu Leu Pro Cys Ala Leu Leu His Arg Leu Leu Arg
109               180             185             190
110
111   CCG GAT GCG CCC GCG CAC CCT CGG TCC CTG GTC CCT TCC GTC CTC CAG      624
112   Pro Asp Ala Pro Ala His Pro Arg Ser Leu Val Pro Ser Val Leu Gln
113               195             200             205
114
115   CGG GAG CGG CGC CCC TGC GGA AGG CCG GGA CTT GGG CAT CGC CTT TAA      672
116   Arg Glu Arg Arg Pro Cys Gly Arg Pro Gly Leu Gly His Arg Leu *
117       210             215             220
118
119
120   (2) INFORMATION FOR SEQ ID NO:2:
121
122         (i) SEQUENCE CHARACTERISTICS:
123               (A) LENGTH: 223 amino acids
124               (B) TYPE: amino acid
125               (D) TOPOLOGY: linear
126
127         (ii) MOLECULE TYPE: protein
128
129         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
130
131   Met Thr Trp Arg His His Val Arg Leu Leu Phe Thr Val Ser Leu Ala
132     1           5               10              15
133
134   Leu Gln Ile Ile Asn Leu Gly Asn Ser Tyr Gln Arg Glu Lys His Asn
135               20              25              30
136
137   Gly Gly Arg Gly Glu Val Thr Lys Val Ala Thr Gln Lys His Arg Gln
138           35              40              45
139
140   Ser Pro Leu Asn Trp Thr Ser Ser His Phe Gly Glu Val Thr Gly Ser
141       50              55              60
142
143   Ala Glu Gly Trp Gly Pro Glu Glu Pro Leu Pro Tyr Ser Arg Ala Phe
144     65              70              75              80
145
146   Gly Glu Gly Ala Ser Ala Arg Pro Arg Cys Cys Arg Asn Gly Gly Thr
147               85              90              95
148
149   Cys Val Leu Gly Ser Phe Cys Val Cys Pro Ala His Phe Thr Gly Arg
150               100             105             110
151
152   Tyr Cys Glu His Asp Gln Arg Arg Ser Glu Cys Gly Ala Leu Glu His
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INPUT SET: S34300.raw

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153              115                120                125
154
155   Gly Ala Trp Thr Leu Arg Ala Cys His Leu Cys Arg Cys Ile Phe Gly
156        130                135                140
157
158   Ala Leu His Cys Leu Pro Leu Gln Thr Pro Asp Arg Cys Asp Pro Lys
159   145                150                155                160
160
161   Asp Phe Leu Ala Ser His Ala His Gly Pro Ser Ala Gly Gly Ala Pro
162                165                170                175
163
164   Ser Leu Leu Leu Leu Leu Pro Cys Ala Leu Leu His Arg Leu Leu Arg
165            180                185                190
166
167   Pro Asp Ala Pro Ala His Pro Arg Ser Leu Val Pro Ser Val Leu Gln
168        195                200                205
169
170   Arg Glu Arg Arg Pro Cys Gly Arg Pro Gly Leu Gly His Arg Leu
171        210                215                220
172
173
174   (2) INFORMATION FOR SEQ ID NO:3:
175
176        (i) SEQUENCE CHARACTERISTICS:
177             (A) LENGTH: 36 base pairs
178             (B) TYPE: nucleic acid
179             (C) STRANDEDNESS: single
180             (D) TOPOLOGY: linear
181
182        (ii) MOLECULE TYPE: DNA (genomic)
183
184
185
186
187        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
188
189   ACTCTTGGAT CCAATTTGGG AAACAGCTAT CAAAGA                        36
190
191   (2) INFORMATION FOR SEQ ID NO:4:
192
193        (i) SEQUENCE CHARACTERISTICS:
194             (A) LENGTH: 42 base pairs
195             (B) TYPE: nucleic acid
196             (C) STRANDEDNESS: single
197             (D) TOPOLOGY: linear
198
199        (ii) MOLECULE TYPE: DNA (genomic)
200
201
202
203
204        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
205
```

INPUT SET: S34300.raw

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206   TACAACTCTA GACTATTATT TACAACATAG AAAATTAAAG GC                     42
207
208   (2) INFORMATION FOR SEQ ID NO:5:
209
210       (i) SEQUENCE CHARACTERISTICS:
211           (A) LENGTH: 36 base pairs
212           (B) TYPE: nucleic acid
213           (C) STRANDEDNESS: single
214           (D) TOPOLOGY: linear
215
216       (ii) MOLECULE TYPE: DNA (genomic)
217
218
219
220
221       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
222
223   ACTCTTGGAT CCGCCATCAT GACCTGGAGG CACCAT                             36
224
225   (2) INFORMATION FOR SEQ ID NO:6:
226
227       (i) SEQUENCE CHARACTERISTICS:
228           (A) LENGTH: 42 base pairs
229           (B) TYPE: nucleic acid
230           (C) STRANDEDNESS: single
231           (D) TOPOLOGY: linear
232
233       (ii) MOLECULE TYPE: DNA (genomic)
234
235
236
237
238       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
239
240   TACAACTCTA GACTATTATT TACAACATAG AAAATTAAAG GC                      42
241
242   (2) INFORMATION FOR SEQ ID NO:7:
243
244       (i) SEQUENCE CHARACTERISTICS:
245           (A) LENGTH: 174 amino acids
246           (B) TYPE: amino acid
247           (C) STRANDEDNESS: single
248           (D) TOPOLOGY: linear
249
250       (ii) MOLECULE TYPE: protein
251
252
253
254
255       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
256
257       Met His Ala Ala Ile Ser Lys Val Phe Glu Leu Gly Leu Val Ala Gly
258       1               5                   10                  15
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/09/393,023A*

INPUT SET: S34300.raw

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